

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 21, 2002, 10:31:33 : Search time 25 Seconds
(without alignments)
793.027 Million cell updates/sec

Title: US-09-943-123-6
Perfect score: 2492
Sequence: 1 MAGVEEVAAGSHLNGDLDP.....XHTILLRPTCKEVSRGDDY 478

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 4147638 residues 112892
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt.40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2468	99.0	478	1 AMP2_HUMAN	P50579 homo sapien
2	2358	94.6	478	1 AMP2_RAT	P38062 rattus norv
3	2348	94.2	478	1 AMP2_MOUSE	O08663 mus musculus
4	1015	40.7	421	1 AMP2_YEAST	P38174 saccharomyc
5	404	16.2	182	1 YD43_CAEEL	P30581 caenorhabdi
6	393	15.8	295	1 AMPM_PYRFU	P36218 pyrococcus
7	375	15.0	295	1 AMPM_PYRHO	O38362 pyrococcus
8	366	14.7	295	1 AMPM_PYRAB	Q9uyt4 pyrococcus
9	347	13.9	294	1 AMPM_METJA	O58725 methanococc
10	307	12.3	291	1 AMPM_ARCFU	O28438 archaeglob
11	295	11.8	299	1 AMPM_METH	O27355 methanobact
12	271.5	10.9	301	1 AMPM_SULSO	P95963 sulfolobus
13	225.5	9.0	394	1 P2G4_HUMAN	Q9uq80 homo sapien
14	225.5	9.0	394	1 P2G4_MOUSE	P50580 mus musculus
15	194.5	7.8	381	1 CDB4_SCHPO	O09184 schizosacch
16	165	6.6	188	1 AMPM_METFE	P22624 methanother
17	145	5.8	712	1 NUCLE_RAT	P13383 rattus norv
18	143	5.7	650	1 NUCLE_XENLA	P20397 xenopus lae
19	140.5	5.6	737	1 PEN_DROME	O61345 drosophila
20	136.5	5.5	1997	1 OTOF_MOUSE	P095f1 mus musculus
21	135.5	5.4	706	1 NUCLE_HUMAN	P19338 homo sapien
22	135	5.4	706	1 NUCLE_MOUSE	P09405 mus musculus
23	135	5.4	1311	1 ATRX_DROME	Q99qns drosophila
24	131	5.3	412	1 FRB4_SPOFR	Q26486 spodoptera
25	128.5	5.2	723	1 SSRP_DROME	Q05344 drosophila
26	126	5.1	767	1 TOP1_CRIGR	Q07050 cricetus
27	124	5.0	1612	1 DNMI_PARLI	Q27746 paracentrot
28	121	4.9	348	1 CYL2_HUMAN	Q14093 homo sapien
29	120.5	4.8	845	1 NFM_MOUSE	P12839 rattus norv
30	119.5	4.8	517	1 T2FA_HUMAN	P35269 homo sapien
31	119	4.8	253	1 AMP1_SYNY3	P53579 synechocyst
32	118.5	4.8	542	1 TUL1_HUMAN	O00294 homo sapien
33	118.5	4.8	1359	1 ATRX_CAEEL	Q9u7e0 caenorhabdi

ALIGNMENTS				
RESULT 1				
ID	AMP2_HUMAN	STANDARD;	PRT;	478 AA.
AC	P50579:			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DE	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Peptidase M 2)			
DE	(Initiation factor 2 associated 67 kDa glycoprotein) (p67) (p67eIF2).			
GN	METAP2 OR MNPEP OR P67EIF2.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=95372350; PubMed=7644482;			
RA	Arfin S.M., Kendall R.B., Hall L., Weaver L.H., Stewart A.E.,			
RA	Matthews B.W., Bradshaw R.A.;			
RT	"Eukaryotic methionyl aminopeptidases: two classes of cobalt-dependent			
RT	enzymes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 92:7714-7718(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Liver;			
RC	MEDLINE=95178556; PubMed=7873610;			
RA	Li X., Chang Y.;			
RT	"Molecular cloning of a human complementary DNA encoding an			
RT	initiation factor 2-associated protein (p67).";			
RL	Biochim. Biophys. Acta 1260:333-336(1995).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 109-478.			
RX	MEDLINE=99030697; PubMed=9812898;			
RA	Liu S., Widom J., Kemp C.W., Crews C.M., Clardy J.;			
RT	"Structure of human methionine aminopeptidase-2 complexed with			
RT	fumagillin.";			
RL	Science 282:1324-1327(1998).			
CC	-!- FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT			
CC	PROTEINS.			
CC	-!- CATALYTIC ACTIVITY: Release of N-terminal amino acids,			
CC	preferentially methionine, from peptides and arylamides.			
CC	-!- COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT (By similarity).			
CC	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24C.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation.			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; U29607; AAA82930.1;			
DR	EMBL; U13261; AAC63402.1;			
DR	PDB; 1B59; 14-JAN-00.			

P08553 mus musculus
Q61587 mus musculus
P08199 mesocricetu
P46872 strongyloce
Q99mr6 mus musculus
P46100 homo sapien
Q01662 saccharomyc
Q28181 bos taurus
P91753 lytechinus
Q28092 bos taurus
Q00203 homo sapien
Q08945 homo sapien

34 118 4.7 848 1 NFM_MOUSE
35 117 4.7 2476 1 ATRX_MOUSE
36 117 4.7 713 1 NUCLE_MESAU
37 116 4.7 699 1 K122_STRPU
38 115.5 4.6 875 1 ARS2_MOUSE
39 115.5 4.6 2492 1 ATRX_HUMAN
40 115 4.6 387 1 AMP1_YEAST
41 115 4.6 1394 1 CNG4_BOVIN
42 114.5 4.6 411 1 MP62_LYTP1
43 114.5 4.6 488 1 CYL2_BOVIN
44 114.5 4.6 1094 1 A3B1_HUMAN
45 114 4.6 709 1 SSRP_HUMAN

DR PDB: 1B6A; 11-JAN-00.
 DR MEROPS: M24_002; .
 DR Genew: HGNC:16672; METAP2.
 DR MIM: 601870; .
 DR InterPro: IPR002468; MAP_2.
 DR InterPro: IPR001714; Methamino_Ptase.
 DR Pfam: PR000994; Peptidase_M24.
 DR PRINTS: PR00557; Peptidase_M24; 1.
 DR TIGRFAMs: TIGR00501; met_pdase_II; 1.
 DR PROSITE: PS01202; MAP_2; 1.
 DR Hydroxylase; Aminopeptidase; Cobalt; 3D-structure.
 KW DOMAIN 36 46 ARG/LYS-RICH (BASIC).
 FT DOMAIN 82 93 ASP/GLU-RICH (ACIDIC).
 FT ACT_SITE 231 231 POLY-LYS.
 FT METAL 231 251 COBALT 2 (BY SIMILARITY).
 FT METAL 262 262 COBALT 1 AND 2 (BY SIMILARITY).
 FT METAL 331 331 COBALT 1 (BY SIMILARITY).
 FT METAL 364 364 COBALT 1 (BY SIMILARITY).
 FT METAL 459 459 COBALT 1 AND 2 (BY SIMILARITY).
 SQ SEQUENCE 478 AA; 52891 MW; 5788E4BB83E48F9A CRC64;

Query Match 99.0%; Score 2468; DB 1; Length 478;
 Best Local Similarity 97.5%; Pred. No. 1e-154;
 Matches 466; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 MAGVEEVAASGSHLNGDLDPDDREGAATAEAAKKRRKKKKSGKSPSAAGEQEPDKES 60
 DB 1 MAGVEEVAASGSHLNGDLDPDDREGAATAEAAKKRRKKKKSGKSPSAAGEQEPDKES 60
 QY 61 GASVDEVARQLERSALEDKERDEDEDDGDDGDDGATGKTKKKKKKKRGPKVQTDPPSPVPI 120
 DB 61 GASVDEVARQLERSALEDKERDEDEDDGDDGDDGATGKTKKKKKKKRGPKVQTDPPSPVPI 120
 QY 121 CDLYPNCVFPKQCEYPPYTDGRTAAWRTTSEKKKALDQASEIWNDFREAAAHQVR 180
 DB 121 CDLYPNCVFPKQCEYPPYTDGRTAAWRTTSEKKKALDQASEIWNDFREAAAHQVR 180
 QY 181 KYNSWIKPGMTWIEICEKLEDGSRKLIKENGSLNAGLXPTGCSLNNCAAXYTPNAGDIT 240
 DB 181 KYNSWIKPGMTWIEICEKLEDGSRKLIKENGSLNAGLXPTGCSLNNCAAXYTPNAGDIT 240
 QY 241 VLQYDDICKTIFGTHISGRILIXCAFTVFNPKYDTLLKAVKDATNTGICAGIDVRLCDV 300
 DB 241 VLQYDDICKTIFGTHISGRILIXCAFTVFNPKYDTLLKAVKDATNTGICAGIDVRLCDV 300
 QY 301 GEAIQWESYEVEIDCKTVQVKPIRXNGXSIQYRXAGKTVPVTKGEATRMEEGEV 360
 DB 301 GEAIQWESYEVEIDCKTVQVKPIRXNGXSIQYRXAGKTVPVTKGEATRMEEGEV 360
 QY 361 YAIXTFGSTGKGVVHDDMECSHYMKNFVGHVPIRLPRTKHLNVLNENFGTLAFCRRLW 420
 DB 361 YAIXTFGSTGKGVVHDDMECSHYMKNFVGHVPIRLPRTKHLNVLNENFGTLAFCRRLW 420
 QY 421 DRIGESKYLMLAKNLCDLGIQVDPXPCDKIGSYTAQFXHTLLRPTCKEVVSRGDDY 478
 DB 421 DRIGESKYLMLAKNLCDLGIQVDPXPCDKIGSYTAQFXHTLLRPTCKEVVSRGDDY 478

RESULT 2
 AMP2_RAT
 ID AMP2_RAT STANDARD; PRT; 478 AA.
 AC P38062;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Peptidase M 2)
 DE (Initiation factor 2 associated 67 kDa glycoprotein) (p67) (p67eif2).
 GN METAP2 OR MNPEP OR P67IF2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

NCBI_TaxID=10116;
 (1)
 SEQUENCE FROM N.A.
 STRAIN-Reuber H35; TISSUE=Liver;
 MEDLINE=93266517; PubMed=8496145;
 RA Wu S., Gupta S., Chatterjee N., Hileman R.E., Kinzy T.G.,
 RA Denslow N.B., Merrick W.C., Chakrabarti D., Osterman J.C., Gupta N.K.;
 RT "Cloning and characterization of complementary DNA encoding the
 RT eukaryotic initiation factor 2-associated 67-kDa protein (p67).";
 RL J. Biol. Chem. 268:10796-10801(1993).
 RN (2)
 REVISIONS TO C-TERMINUS.
 RP MEDLINE=95372350; PubMed=7644482;
 RA Arfin S.M., Kendall R.L., Hall L., Weaver L.H., Stewart A.E.,
 RA Matthews B.W., Bradshaw R.A.;
 RT "Eukaryotic methionyl aminopeptidases: two classes of
 RT cobalt-dependent enzymes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7714-7718(1995).
 CC -!- FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT
 CC PROTEINS.
 CC -!- FUNCTION: PROTECTS EIF-2 ALPHA-SUBUNIT FROM INHIBITORY
 CC PHOSPHORYLATION BY EIF-2 KINASES. PLAYS A CRITICAL ROLE IN THE
 CC REGULATION OF PROTEIN SYNTHESIS. IT ALSO INTERACTS WITH THE
 CC EIF-2 GAMMA-SUBUNIT.
 CC -!- CATALYTIC ACTIVITY: Release of N-terminal amino acids,
 CC preferentially methionine, from peptides and arylamides.
 CC -!- COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT (BY SIMILARITY).
 CC -!- PFM: CONTAINS 12 O-LINKED GLNAC.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24C.
 CC -----
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 CC -----
 CC EMBL: L10652; AAA41111.1;
 DR PIR: A46702; A46702.
 DR HSP: P50579; 1B6A.
 DR MEROPS: M24_002;
 DR InterPro: IPR002468; MAP_2.
 DR InterPro: IPR001714; Methamino_Ptase.
 DR InterPro: IPR000994; Peptidase_M24.
 DR Pfam: PF00557; Peptidase_M24; 1.
 DR PRINTS: PR00559; MAPEPTIDASE.
 DR TIGRFAMs: TIGR00501; met_pdase_II; 1.
 DR PROSITE: PS01202; MAP_2; 1.
 KW Hydroxylase; Aminopeptidase; Cobalt; Glycoprotein.
 FT DOMAIN 36 46 ARG/LYS-RICH (BASIC).
 FT DOMAIN 82 93 ASP/GLU-RICH (ACIDIC).
 FT METAL 251 251 POLY-LYS.
 FT METAL 262 262 COBALT 2 (BY SIMILARITY).
 FT METAL 331 331 COBALT 1 AND 2 (BY SIMILARITY).
 FT METAL 364 364 COBALT 1 (BY SIMILARITY).
 FT METAL 459 459 COBALT 1 AND 2 (BY SIMILARITY).
 FT CONFLICT 464 478 LRPTCKEVVSRGDDY -> CAQPKKLSAEWTIKT (IN REF. 1).
 SQ SEQUENCE 478 AA; 53052 MW; BEIC0E91E0CB3D74 CRC64;

Query Match 94.6%; Score 2358; DB 1; Length 478;
 Best Local Similarity 92.5%; Pred. No. 1.6e-147;
 Matches 442; Conservative 10; Mismatches 26; Indels 0; Gaps 0;

QY 1 MAGVEEVAASGSHLNGDLDPDDREGAATAEAAKKRRKKKKSGKSPSAAGEQEPDKES 60
 DB 1 MAGVEEVAASGSHLNGDLDPDDREGAATAEAAKKRRKKKKSGKSPSAAGEQEPDKES 60
 QY 61 GASVDEVARQLERSALEDKERDEDEDDGDDGDDGATGKTKKKKKKKRGPKVQTDPPSPVPI 120
 DB 61 GTSVDEVAKOLEROALBEKEKDDDDGDDGDDGACGAKKKKKKKKKRGPKVQTDPPSPVPI 120

KKKRGPVKVOTDPPSPVPCIDLYPNVGFPPKQCEYPPPTDGRTAARRTTSBEKALDO
 ASEEIWNDFREAAHROVRYMSWIKPMGTMIIEICKLEDCSKLICKENGLAGLA
 PPTGSLNNCAHRTYVNGADTVLOYDDICKIDFGTHISGRIDICAFVTPNPKYDYL
 LKAVKDATNTAKIGIDVRLCDVGEATQEVMESEYVEIDGKYQVQKRLNLSHIG
 QYRIHAGKTVPVIVKGEATRMEEGVEVVALETFTSGKGVVHDDMECSHYMKNFVGHV
 PIRLPTKHLNINENFCTLAFPRWLDRLGESKYLMALKNLCDLIGVDPPIPLCDI
 KGSYTAQPEHTILLRPTCKEVVSRGDDY*
 BASE COUNT 957 a 466 c 542 g 602 t
 ORIGIN

Query Match	Score	1432.8	DB 9	Length	2569
Best Local Similarity	99.7%				
Mismatches	0				
Indels	3				
Gaps	0				
1	ATGGCGGGCGTGGAGAGGTAGCGCCCTCCGGGAGCCACCTGAATGGGACCTGGATCCA	60			
23	ATGGCGGGCGTGGAGAGGTAGCGCCCTCCGGGAGCCACCTGAATGGGACCTGGATCCA	82			
61	GACGACAGGAGACAGGAGCTGCTCTACGGCTGAGGAAGCAGCCCAAGAAAAAGACGA	120			
83	GACGACAGGAGAGAGAGCTGCTCTACGGCTGAGGAAGCAGCCCAAGAAAAAGACGA	142			
121	AGCAAGAGAGAGAGAGAGCTGCTCTACGGCTGAGGAAGCAGCCCAAGAAAAAGATCA	180			
143	AGCAAGAGAGAGAGAGAGCTGCTCTACGGCTGAGGAAGCAGCCCAAGAAAAAGATCA	202			
181	GGAGCCTCAGTGGATGAAGTAGCAAGACAGTTGGAAGATCAGCATTTGGAAGATAAGAA	240			
203	GGAGCCTCAGTGGATGAAGTAGCAAGACAGTTGGAAGATCAGCATTTGGAAGATAAGAA	262			
241	AGAGATGAAGATGATGAAGTAGCAAGACAGTTGGAAGATCAGCATTTGGAAGATAAGAA	300			
263	AGAGATGAAGATGATGAAGTAGCAAGACAGTTGGAAGATCAGCATTTGGAAGATAAGAA	322			
301	AAAAAGAGAGAGAGAGAGCTGCTCTACGGCTGAGGAAGCAGCCCAAGAAAAAGATCA	360			
323	AAAAAGAGAGAGAGAGAGCTGCTCTACGGCTGAGGAAGCAGCCCAAGAAAAAGATCA	382			
361	TGTGACCTGTATCTTAATGTGTATTTCCCAAGAGAGAGAGCTGCTCTACGGCTGAGGA	420			
383	TGTGACCTGTATCTTAATGTGTATTTCCCAAGAGAGAGAGCTGCTCTACGGCTGAGGA	442			
421	CAAGATGGCGGACAGCTGCTTGGAGAACTACAAAGTGAAGAAAGAAAGATTTAGATCAG	480			
443	CAAGATGGCGGACAGCTGCTTGGAGAACTACAAAGTGAAGAAAGAAAGATTTAGATCAG	502			
481	GCAAGTGAAGAGATTTGAATGATTTTCGAGAAGCTGCGAAGCAGCATCGACAAGTTGA	540			
503	GCAAGTGAAGAGATTTGAATGATTTTCGAGAAGCTGCGAAGCAGCATCGACAAGTTGA	562			
541	AAATAGCTTAATGAGCTGGATCAAGCTTGGATGAAGATGATGAAGATTTGGAAGTTG	600			
563	AAATAGCTTAATGAGCTGGATCAAGCTTGGATGAAGATGATGAAGATTTGGAAGTTG	622			
601	GAAGACTGTTTCAGCGAAGTTAATAAGAGAGATGGAATTAATGCGAGCTGGCATTTCT	660			
623	GAAGACTGTTTCAGCGAAGTTAATAAGAGAGATGGAATTAATGCGAGCTGGCATTTCT	682			
661	ACTGGATGTTCTCTCAATANTTGTGCTGCGCCTATCTCCCAATGCGGCTGACACAACA	720			
683	ACTGGATGTTCTCTCAATANTTGTGCTGCGCCTATCTCCCAATGCGGCTGACACAACA	742			
721	GTATTACAGTATGATGACATCTGTAAATAGACTTTTGGACACATATAAGTGGTAGGATT	780			
743	GTATTACAGTATGATGACATCTGTAAATAGACTTTTGGACACATATAAGTGGTAGGATT	802			
781	ATTGACTGTGCTTTTACTGTCACTTTTAAATCCCAATATGATGATTTTAAAGCTGTA	840			
803	ATTGACTGTGCTTTTACTGTCACTTTTAAATCCCAATATGATGATTTTAAAGCTGTA	862			
841	AAAGATGCTACTAAACACTGGATGAAGTGTGCTGGAATTTGTTGCTGTGTGATGTT	900			
863	AAAGATGCTACTAAACACTGGATGAAGTGTGCTGGAATTTGTTGCTGTGTGATGTT	922			

QY	901	GGTGGGCGCATCCAAGAGTTTATGGAGTCTCTATGAAGTTGAATAGATGGGAGACATAT	960
DB	923	GGTGGGCGCATCCAAGAGTTTATGGAGTCTCTATGAAGTTGAATAGATGGGAGACATAT	982
QY	961	CAAGTGAACCAATCCGTAATCTAAATGACATTCATTAATGGGCAATATAGAATACATGCT	1020
DB	983	CAAGTGAACCAATCCGTAATCTAAATGACATTCATTAATGGGCAATATAGAATACATGCT	1042
QY	1021	GGAAAAACAGTGGCGGATTTGTAAGAGGAGGAGGCAACAAAGATGGAGGAGGAGTA	1080
DB	1043	GGAAAAACAGTGGCGGATTTGTAAGAGGAGGAGGCAACAAAGATGGAGGAGGAGTA	1102
QY	1081	TATGCAATTTGAACCTTTTGGTAGTACAGAAAAAGGTGTTTTCATGATGATGATGATGAT	1140
DB	1103	TATGCAATTTGAACCTTTTGGTAGTACAGAAAAAGGTGTTTTCATGATGATGATGATGAT	1162
QY	1141	TCACATTACATGAAAAATTTTTCATGTTGACATGTGCCAATAGGCTTCCCAAGAACAAA	1200
DB	1163	TCACATTACATGAAAAATTTTTCATGTTGACATGTGCCAATAGGCTTCCCAAGAACAAA	1222
QY	1201	CACCTTTAAATGTCATCAATGAAACTTTTGAACCTTTTGAACCTTTTGAACCTTTTGA	1260
DB	1223	CACCTTTAAATGTCATCAATGAAACTTTTGAACCTTTTGAACCTTTTGAACCTTTTGA	1282
QY	1261	GATCGCTTGGGAGAAAGTAATTAATCTTGCATGCTGAGAACTTCTGCTGACTTTGGCAT	1320
DB	1283	GATCGCTTGGGAGAAAGTAATTAATCTTGCATGCTGAGAACTTCTGCTGACTTTGGCAT	1342
QY	1321	GTACATCCATATCCACCATTTATGTGACATTAAGAGATCATATACAGGCAATTTGAACAT	1380
DB	1343	GTACATCCATATCCACCATTTATGTGACATTAAGAGATCATATACAGGCAATTTGAACAT	1402
QY	1381	ACCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1437
DB	1403	ACCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1459

RESULT 3
 G28539 human STS SHGC-31600, sequence tagged site.
 LOCUS G28539
 DEFINITION G28539, 1 GI:1408354
 ACCESSION G28539, 1
 VERSION STS; STS sequence; primer; sequence tagged site.
 KEYWORDS Homo sapiens.
 SOURCE Eukaryota; Metazoa; Chordata; Cranial; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 ORGANISM
 REFERENCE
 AUTHORS
 JOURNAL
 COMMENT
 Contact: Richard M. Myers
 Stanford Human Genome Center (SHGC)
 Stanford University School of Medicine
 Department of Genetics, M-344, Stanford, CA 94305, USA
 Tel: 415/7259687
 Fax: 415/7259689
 Email: myers@shgc.stanford.edu
 Primer A: CAAAGCCACCTCAACACCTT
 Primer B: AGGAAGGGGAAAAACAGTAGC
 STS size: 216
 PCR Profile:
 Initial incubation: 94 degrees C for 90 seconds
 Denaturation: 94 degrees C for 15 seconds
 Annealing: 62 degrees C for 23 seconds
 Polymerization: 72 degrees C for 30 seconds
 PCR Cycles: 30
 Thermal Cycler: Perkin Elmer 9600
 Protocol:

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OM protein - protein search, using sw model

Run on: December 21, 2002, 10:31:33 ; Search time 25 Seconds
(without alignments)
793.027 Million cell updates/sec

Title: US-09-943-123-6
Perfect score: 2492
Sequence: 1 MAGVEEVAASGSLHGLDLP.....XHTLLRPTCKEVVSRGDDY 478

Scoring table: BLOSUM62
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Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt_40:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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10	307	12.3	291	1 AMPM_ARCFU	O27355 methanobact
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14	225.5	9.0	394	1 P2G4_MOUSE	O09184 schizosacch
15	194.5	7.8	381	1 CDB4_SCHPO	P22624 methanother
16	165	6.6	188	1 AMPM_METFE	P13383 rattus norv
17	145	5.8	712	1 NUCLE_RAT	P20397 xenopus lae
18	143	5.7	650	1 NUCLE_XENLA	O61345 drosophila
19	140.5	5.6	737	1 PEN_DROME	O9est1 mus musculu
20	136.5	5.5	1997	1 OTOF_MOUSE	P19338 homo sapien
21	135.5	5.4	706	1 NUCLE_HUMAN	P09405 mus musculu
22	135	5.4	706	1 NUCLE_MOUSE	O9eqn5 drosophila
23	135	5.4	1311	1 ATRX_DROME	O26486 spodoptera
24	131	5.3	412	1 FKBA_SPOFR	O05344 drosophila
25	128.5	5.2	723	1 SSRP_DROME	O07050 cricetus
26	126	5.1	767	1 TOP1_CRIGR	O27746 paracentrot
27	124	5.0	1612	1 DNML_PARLI	Q14093 homo sapien
28	121	4.9	348	1 CYL2_HUMAN	P12839 rattus norv
29	120.5	4.8	845	1 NFM_RAT	P35269 homo sapien
30	119.5	4.8	517	1 T2FA_HUMAN	P53579 synechocyst
31	119	4.8	253	1 AMPL_SYNY3	O00294 homo sapien
32	118.5	4.8	542	1 TULL_HUMAN	Q9u7e0 caenorhabdi
33	118.5	4.8	1359	1 ATRX_CAEEL	

34	118	4.7	848	1 NFM_MOUSE	P08553 mus musculu
35	118	4.7	2476	1 ATRX_MOUSE	Q01687 mus musculu
36	117	4.7	713	1 NUCLE_MESAU	P08199 mesocricetu
37	116	4.7	699	1 KI22_STRPU	P46872 strongyloce
38	115.5	4.6	875	1 ARS2_MOUSE	O59mr6 mus musculu
39	115.5	4.6	2492	1 ATRX_HUMAN	P46100 homo sapien
40	115	4.6	387	1 AMPL_YEAST	Q01662 saccharomyc
41	115	4.6	1394	1 CNG4_BOVIN	Q28181 bos taurus
42	114.5	4.6	411	1 MP62_LYTP1	P91753 lytechinus
43	114.5	4.6	488	1 CYL2_BOVIN	Q28092 bos taurus
44	114.5	4.6	1094	1 A3BL_HUMAN	O00203 homo sapien
45	114	4.6	709	1 SSRP_HUMAN	Q08945 homo sapien

ALIGNMENTS

RESULT 1
AMP2_HUMAN
ID AMP2_HUMAN STANDARD: PRT: 478 AA.
AC P50579:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Peptidase M 2)
DE (Initiation factor 2 associated 67 kDa glycoprotein) (p67) (p67eif2).
GN METAP2 OR MNPEP OR p67eif2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95372350; PubMed=7644482;
RA Arfin S.M., Kendall R.L., Hall L., Weaver L.H., Stewart A.E.,
RA Matthews B.W., Bradshaw R.A.;
RT "Eukaryotic methionyl aminopeptidases: two classes of cobalt-dependent
enzymes";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7714-7718(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95178556; PubMed=7873610;
RA Li X., Chang Y.;
RT "Molecular cloning of a human complementary DNA encoding an
initiation factor 2-associated protein (p67).";
RL Biochim. Biophys. Acta 1260:333-336(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 109-478.
RX MEDLINE=99030697; PubMed=9812898;
RA Liu S., Widom J., Kemp C.W., Crews C.M., Clardy J.;
RT "Structure of human methionine aminopeptidase-2 complexed with
fumagillin.";
RL Science 282:1324-1327(1998).
CC -!- FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT
PROTEINS.
CC -!- CATALYTIC ACTIVITY: Release of N-terminal amino acids,
preferentially methionine, from peptides and arylamides.
CC -!- COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT (By similarity).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24C.
CC -----
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CC -----
CC EMBL; U29607; AAA82930.1; -
DR EMBL; U13261; AAC63402.1; -
DR PDB; 1B59; 14-JAN-00.

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DR PDB: 1B6A; 11-JAN-00.
DR MEROPS; M24.002; -.
DR Genew; HGNC:16672; METAP2.
DR MIM; 601870; -.
DR InterPro; IPR002468; MAP_2.
DR InterPro; IPR001714; Methamino_Ptase.
DR InterPro; IPR000994; Peptidase_M24.
DR Pfam; PF00557; Peptidase_M24; 1.
DR PRINTS; PR00599; MAPEPTIDASE.
DR TIGRFAMs; TIGR00501; met_pdase-II; 1.
DR PROSITE; PS01202; MAP_2; 1.
DR Hydrolase; AminoPeptidase; Cobalt; 3D-structure.
KW DOMAIN 36 46 ARG/LYS-RICH (BASIC).
FT DOMAIN 82 93 ASP/GLU-RICH (ACIDIC).
FT ACT_SITE 231 231 POLY-LYS.
FT METAL 251 251 COBALT 2 (BY SIMILARITY).
FT METAL 262 262 COBALT 1 AND 2 (BY SIMILARITY).
FT METAL 331 331 COBALT 1 (BY SIMILARITY).
FT METAL 364 364 COBALT 1 (BY SIMILARITY).
FT METAL 459 459 COBALT 1 AND 2 (BY SIMILARITY).
SQ SEQUENCE 478 AA; 52891 MW; 5788E4B83E48F9A CRC64;

Query Match 99.0%; Score 2468; DB 1; Length 478;
Best Local Similarity 97.5%; Pred. No. 1e-154;
Matches 466; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 MAGVEEVAASGSHLGLDLPDDREEGAATAEAAKRRKKKSKGSAAGQEPDKES 60
DB 1 MAGVEEVAASGSHLGLDLPDDREEGAATAEAAKRRKKKSKGSAAGQEPDKES 60

QY 61 GASVDEVARQLERSALEDEKEDDEDGDDGDDGATGKTKKRRKKKRGPKVQTDPPSVPI 120
DB 61 GASVDEVARQLERSALEDEKEDDEDGDDGDDGATGKTKKRRKKKRGPKVQTDPPSVPI 120

QY 121 CDLYPNGVFPKQCEYPTDGRTAARWTTSEKKALDOASEEINWDPREAAEAHQVR 180
DB 121 CDLYPNGVFPKQCEYPTDGRTAARWTTSEKKALDOASEEINWDPREAAEAHQVR 180

QY 181 KYVMSWIKPGMTMIEICEKLEDCSKLTKENGLNAGLAXPTGCSLNCAAXYTPNAGDTT 240
DB 181 KYVMSWIKPGMTMIEICEKLEDCSKLTKENGLNAGLAFPTGCSLNCAAHYTPNAGDTT 240

QY 241 VLQYDDICKIXFGTHISGRITXCAFTVFNPKYDTLLKAVKDATNTGKICAGIDVRLCDV 300
DB 241 VLQYDDICKIDFGTHISGRITDCAFTVFNPKYDTLLKAVKDATNTGKICAGIDVRLCDV 300

QY 301 GEATQEWSEYEIDGKTYQVKPIRNKXGXSIGQYRXAGKTYPIVKGGEATRMEEGEV 360
DB 301 GEATQEWSEYEVEIDGKTYQVKPIRNKXGXSIGQYRIHAGKTYPIVKGGEATRMEEGEV 360

QY 361 YAIYFTGSGVGVHDDMECSHYMKNFVDGHPVIRLPRTKHLLNVIENFGTLAFCRWL 420
DB 361 YAIYFTGSGVGVHDDMECSHYMKNFVDGHPVIRLPRTKHLLNVIENFGTLAFCRWL 420

QY 421 DRLGESKYLKALKNLCDLGIVDPXPXCDIKGVSQAQFXHTILLRPTCKEVSRGDDY 478
DB 421 DRLGESKYLKALKNLCDLGIVDPYPLCDINGSTIAQFHTILLRPTCKEVSRGDDY 478

RESULT 2
AMP2_RAT ID AMP2_RAT STANDARD; PRT; 478 AA.
AC P38062;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Peptidase M 2)
GN (Initiation factor 2 associated 67 kDa glycoprotein) (p67) (p67eIF2).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Reuber H35; TISSUE=Liver;
RX MEDLINE=93266517; PubMed=8496145;
RA Wu S., Gupta S., Chatterjee N., Hileman R.E., Kinzy T.G.,
RA Denslow N.D., Merrick W.C., Chakrabarti D., Osterman J.C., Gupta N.K.;
RT "Cloning and characterization of complementary DNA encoding the
RL eukaryotic initiation factor 2-associated 67-kDa protein (p67).";
RL J. Biol. Chem. 268:10796-10801(1993).
RN [2]
RP REVISIONS TO C-TERMINUS
RX MEDLINE=95372350; PubMed=7644482;
RA Arfin S.M., Kendall R.L., Hall L., Weaver L.H., Stewart A.E.,
RA Matthews B.W., Bradshaw R.A.;
RT "Eukaryotic methionyl aminopeptidases: two classes of
RT cobalt-dependent enzymes.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7714-7718(1995).
CC -1- FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT
CC PROTEINS.
CC -1- FUNCTION: PROTECTS EIF-2 ALPHA-SUBUNIT FROM INHIBITORY
CC PHOSPHORYLATION BY EIF-2 KINASES. PLAYS A CRITICAL ROLE IN THE
CC REGULATION OF PROTEIN SYNTHESIS. IT ALSO INTERACTS WITH THE
CC EIF-2 GAMMA-SUBUNIT.
CC -1- CATALYTIC ACTIVITY: Release of N-terminal amino acids,
CC preferentially methionine, from peptides and arylamides.
CC -1- COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT (BY SIMILARITY).
CC -1- PTM: CONTAINS 12 O-LINKED GLCNAC.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24C.
CC
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CC -----
CC EMBL; LI0652; AAA11111.1; -.
CC PIR; A46702; A46702.
CC HSSP; P50579; 1B6A.
CC MEROPS; M24.002; -.
CC InterPro; IPR002468; MAP_2.
CC InterPro; IPR001714; Methamino_Ptase.
CC InterPro; IPR000994; Peptidase_M24.
CC Pfam; PF00557; Peptidase_M24; 1.
CC PRINTS; PR00599; MAPEPTIDASE.
CC TIGRFAMs; TIGR00501; met_pdase-II; 1.
CC PROSITE; PS01202; MAP_2; 1.
CC Hydrolase; AminoPeptidase; Cobalt; Glycoprotein.
KW DOMAIN 36 46 ARG/LYS-RICH (BASIC).
FT DOMAIN 82 93 ASP/GLU-RICH (ACIDIC).
FT METAL 251 251 POLY-LYS.
FT METAL 262 262 COBALT 2 (BY SIMILARITY).
FT METAL 331 331 COBALT 1 AND 2 (BY SIMILARITY).
FT METAL 364 364 COBALT 1 (BY SIMILARITY).
FT METAL 459 459 COBALT 1 (BY SIMILARITY).
FT METAL 464 478 COBALT 1 AND 2 (BY SIMILARITY).
FT CONFLICT 464 478 LPTCKEVSRGDDY -> CAQPVKKLSAEWTKT (IN
FT REF. 1).
SQ SEQUENCE 478 AA; 53052 MW; BEIC0E91E0CB3D74 CRC64;

Query Match 94.6%; Score 2358; DB 1; Length 478;
Best Local Similarity 92.5%; Pred. No. 1.6e-147;
Matches 442; Conservative 10; Mismatches 26; Indels 0; Gaps 0;

QY 1 MAGVEEVAASGSHLGLDLPDDREEGAATAEAAKRRKKKSKGSAAGQEPDKES 60
DB 1 MAGVEEVAASGSHLGLDLPDDREEGAATAEAAKRRKKKSKGSAAGQEPDKES 60

QY 61 GASVDEVARQLERSALEDEKEDDEDGDDGDDGATGKTKKRRKKKRGPKVQTDPPSVPI 120
DB 61 GASVDEVARQLERSALEDEKEDDEDGDDGDDGATGKTKKRRKKKRGPKVQTDPPSVPI 120

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protocol: